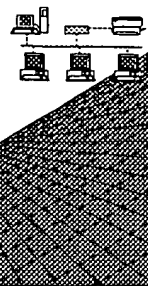


Huff

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



FILE COPY

#12

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/833506A
Art Unit / Team No. : 1642
Date Processed by STIC: 3/29/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

08/833,506A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

FILE COPY

S. HUFF

1642

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999
TIME: 08:48:08

INPUT SET: S31225.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

*Important:
See item 5
on Error Summary
sheet*

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: ROBERT WEBBER
5 (ii) TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL ANTIBODY REACT?
6 (iii) NUMBER OF SEQUENCES: 126
7 (iv) CORRESPONDENCE ADDRESS:
8 (A) ADDRESSEE: BIELEN, PETERSON & LAMPE
9 (B) STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
10 (C) CITY: WALNUT CREEK
11 (D) STATE: CALIFORNIA
12 (E) COUNTRY: UNITED STATES OF AMERICA
13 (F) ZIP: 94596
14 (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: DISKETTE 3.5 INCH, 1.44 MB FOR FORMATTED
16 (B) COMPUTER: IBM PC COMPATIBLE
17 (C) OPERATING SYSTEM: DOS
18 (D) SOFTWARE: WORDPERFECT 5.1
19 (vi) CURRENT APPLICATION DATA:
20 (A) APPLICATION NUMBER: NONE
21 (B) FILING DATE: NONE
22 (C) CLASSIFICATION:
23 (vii) PRIOR APPLICATION DATA:
24 (A) APPLICATION NUMBER: 08/634,332
25 (B) FILING DATE: 12 APRIL 1996
26 (viii) ATTORNEY/AGENT INFORMATION:
27 (A) NAME: THEODORE J. BIELEN, JR.
28 (B) REGISTRATION NUMBER: 27,420
29 (C) REFERENCE/DOCKET NUMBER: 12280
30 (ix) TELECOMMUNICATION INFORMATION:
31 (A) TELEPHONE: (925) 937-1515
32 (B) TELEFAX: (925) 937-1529
33
34

*Does Not Comply
Corrected Diskette Needed*

--> *α*

ERRORED SEQUENCES FOLLOW:

35 (2) INFORMATION FOR SEQ ID NO: 1:
36 (i) SEQUENCE CHARACTERISTICS:
37 (A) LENGTH: 18
38 (B) TYPE: AMINO ACID
39 (D) TOPOLOGY: LINEAR

-->

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:09

INPUT SET: S31225.raw

40 (ii) MOLECULE TYPE: PEPTIDE
41 (ix) FEATURE:
42 (A) NAME/KEY: HUMAN iNOS (25-42)
43 (B) LOCATION:
44 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
45 (D) OTHER INFORMATION:
46
47
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
49
--> 50 AsnAsnAsnValGluLysAlaProCysAlaThrSerSer
51 510
--> 52 ProValThrGlnAsp
53 15
54
55

*This is due to the use of
TAB codes between amino
acids and between amino
acid numbers. Use space
character instead.*

56 (2) INFORMATION FOR SEQ ID NO: 2:
57 (i) SEQUENCE CHARACTERISTICS:
--> 58 (A) LENGTH: 18
59 (B) TYPE: AMINO ACID
60 (D) TOPOLOGY: LINEAR
61 (ii) MOLECULE TYPE: PEPTIDE
62 (ix) FEATURE:
63 (A) NAME/KEY: MOUSE iNOS (25-42)
64 (B) LOCATION:
65 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
66 (D) OTHER INFORMATION:
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
68
--> 69 AsnAsnAsnValLysLysThrProCysAlaValLeuSer
70 510
--> 71 ProThrIleGlnAsp
72 15
73
74

(global error)

same error

75 (2) INFORMATION FOR SEQ ID NO: 3:
76 (i) SEQUENCE CHARACTERISTICS:
--> 77 (A) LENGTH: 18
78 (B) TYPE: AMINO ACID
79 (D) TOPOLOGY: LINEAR
80 (ii) MOLECULE TYPE: PEPTIDE
81 (ix) FEATURE:
82 (A) NAME/KEY: RAT iNOS (25-42)
83 (B) LOCATION:
84 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
85 (D) OTHER INFORMATION:
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
87
--> 88 AsnAsnAsnValGluLysThrProGlyAlaIleProSer
89 510
--> 90 ProThrThrGlnAsp

same

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:09

INPUT SET: S31225.raw

91 15
92
93

94 (2) INFORMATION FOR SEQ ID NO: 4:
95 (i) SEQUENCE CHARACTERISTICS:
--> 96 (A) LENGTH: 18
97 (B) TYPE: AMINO ACID
98 (D) TOPOLOGY: LINEAR
99 (ii) MOLECULE TYPE: PEPTIDE
100 (ix) FEATURE:
101 (A) NAME/KEY: HUMAN iNOS (37-54)
102 (B) LOCATION:
103 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
104 (D) OTHER INFORMATION:
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
106
--> 107 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
108 510
--> 109 SerLysGlnGlnAsn
110 15
111
112

113 (2) INFORMATION FOR SEQ ID NO: 5:
114 (i) SEQUENCE CHARACTERISTICS:
--> 115 (A) LENGTH: 18
116 (B) TYPE: AMINO ACID
117 (D) TOPOLOGY: LINEAR
118 (ii) MOLECULE TYPE: PEPTIDE
119 (ix) FEATURE:
120 (A) NAME/KEY: HUMAN iNOS (781-798)
121 (B) LOCATION:
122 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
123 (D) OTHER INFORMATION:
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
125
--> 126 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
127 510
--> 128 GlyProThrProHis
129 15
130
131

132 (2) INFORMATION FOR SEQ ID NO: 6:
133 (i) SEQUENCE CHARACTERISTICS:
--> 134 (A) LENGTH: 17
135 (B) TYPE: AMINO ACID
136 (D) TOPOLOGY: LINEAR
137 (ii) MOLECULE TYPE: PEPTIDE
138 (ix) FEATURE:
139 (A) NAME/KEY: MOUSE iNOS (776-792)
140 (B) LOCATION:

same

✓

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:09

INPUT SET: S31225.raw

141 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
142 (D) OTHER INFORMATION:
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
144
--> 145 XaaAlaLeuValGlnGlyIleLeuGluArgValValAsp
146 510
--> 147 CysProThrProHis
148 15
149
150
151

152 (2) INFORMATION FOR SEQ ID NO: 7:
153 (i) SEQUENCE CHARACTERISTICS:
--> 154 (A) LENGTH: 15
155 (B) TYPE: AMINO ACID
156 (D) TOPOLOGY: LINEAR
157 (ii) MOLECULE TYPE: PEPTIDE
158 (ix) FEATURE:
159 (A) NAME/KEY: RAT iNOS (780-794)
160 (B) LOCATION:
161 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
162 (D) OTHER INFORMATION:
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
164
--> 165 XaaXaaLeuValGlnGlyIleLeuGluArgValValAsp
166 510
--> 167 CysSerSerProXaa
168 15
169
170

171 (2) INFORMATION FOR SEQ ID NO: 8:
172 (i) SEQUENCE CHARACTERISTICS:
--> 173 (A) LENGTH: 18
174 (B) TYPE: AMINO ACID
175 (D) TOPOLOGY: LINEAR
176 (ii) MOLECULE TYPE: PEPTIDE
177 (ix) FEATURE:
178 (A) NAME/KEY: HUMAN iNOS (985-1002)
179 (B) LOCATION:
180 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
181 (D) OTHER INFORMATION:
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
183
--> 184 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
185 510
--> 186 HisAspSerGlnHis
187 15
188
189

190 (2) INFORMATION FOR SEQ ID NO: 9:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:10

INPUT SET: S31225.raw

--> 191 (i) SEQUENCE CHARACTERISTICS:
192 (A) LENGTH: 18
193 (B) TYPE: AMINO ACID
194 (D) TOPOLOGY: LINEAR
195 (ii) MOLECULE TYPE: PEPTIDE
196 (ix) FEATURE:
197 (A) NAME/KEY: MOUSE iNOS (978-995)
198 (B) LOCATION:
199 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
200 (D) OTHER INFORMATION:
201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
202
203
--> 204 GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu
205 510
--> 206 HisAspSerGlnHis
207 15
208
209

210 (2) INFORMATION FOR SEQ ID NO: 10:
211 (i) SEQUENCE CHARACTERISTICS:
--> 212 (A) LENGTH: 18
213 (B) TYPE: AMINO ACID
214 (D) TOPOLOGY: LINEAR
215 (ii) MOLECULE TYPE: PEPTIDE
216 (ix) FEATURE:
217 (A) NAME/KEY: RAT iNOS (982-998)
218 (B) LOCATION:
219 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
220 (D) OTHER INFORMATION:
221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
222
--> 223 GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu510
--> 224 HisAspSerGlnHis
225 15
226
227

228 (2) INFORMATION FOR SEQ ID NO: 11:
229 (i) SEQUENCE CHARACTERISTICS:
--> 230 (A) LENGTH: 18
231 (B) TYPE: AMINO ACID
232 (D) TOPOLOGY: LINEAR
233 (ii) MOLECULE TYPE: PEPTIDE
234 (ix) FEATURE:
235 (A) NAME/KEY: HUMAN nNOS (1256-1273)
236 (B) LOCATION:
237 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
238 (D) OTHER INFORMATION:
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
240
--> 241 GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln

same

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999

TIME: 08:48:10

INPUT SET: S31225.raw

--> 242 510
243 PheAspIleGlnHis
244 15
245
246

same

247 (2) INFORMATION FOR SEQ ID NO: 12:
248 (i) SEQUENCE CHARACTERISTICS:
--> 249 (A) LENGTH: 15
250 (B) TYPE: AMINO ACID
251 (D) TOPOLOGY: LINEAR
252 (ii) MOLECULE TYPE: PEPTIDE
253 (ix) FEATURE:
254 (A) NAME/KEY: HUMAN eNOS (1017-1031)
255 (B) LOCATION:
256 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
257 (D) OTHER INFORMATION:
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
259
--> 260 GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
261 510
--> 262 HisAspXaaXaaXaa
263 15
264
265

266 (2) INFORMATION FOR SEQ ID NO: 13:
267 (i) SEQUENCE CHARACTERISTICS:
--> 268 (A) LENGTH: 15
269 (B) TYPE: AMINO ACID
270 (D) TOPOLOGY: LINEAR
271 (ii) MOLECULE TYPE: PEPTIDE
272 (ix) FEATURE:
273 (A) NAME/KEY: BOVINE eNOS (1019-1033)
274 (B) LOCATION:
275 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
276 (D) OTHER INFORMATION:
277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
278
--> 279 GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
280 510
--> 281 HisAspXaaXaaXaa
282 15
283
284

285 (2) INFORMATION FOR SEQ ID NO: 14:
286 (i) SEQUENCE CHARACTERISTICS:
--> 287 (A) LENGTH: 18
288 (B) TYPE: AMINO ACID
289 (D) TOPOLOGY: LINEAR
290 (ii) MOLECULE TYPE: PEPTIDE
291 (ix) FEATURE:

✓

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:10

INPUT SET: S31225.raw

292 (A) NAME/KEY: HUMAN iNOS (1009-1026)
293 (B) LOCATION:
294 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
295 (D) OTHER INFORMATION:
296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
297
--> 298 ArgMetThrLeuValPheGlyCysArgArgProAspGlu
299 510
--> 300 AspHisIleTyrGln
301 15
302
303

304 (2) INFORMATION FOR SEQ ID NO: 15:
305 (i) SEQUENCE CHARACTERISTICS:
--> 306 (A) LENGTH: 18
307 (B) TYPE: AMINO ACID
308 (D) TOPOLOGY: LINEAR
309 (ii) MOLECULE TYPE: PEPTIDE
310 (ix) FEATURE:
311 (A) NAME/KEY: RAT iNOS (1006-1023)
312 (B) LOCATION:
313 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
314 (D) OTHER INFORMATION:
315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
316
--> 317 ArgMetThrLeuValPheGlyCysArgHisProGluGlu
318 510
--> 319 AspHisLeuTyrGln
320 15
321
322

323 (2) INFORMATION FOR SEQ ID NO: 16:
324 (i) SEQUENCE CHARACTERISTICS:
--> 325 (A) LENGTH: 18
326 (B) TYPE: AMINO ACID
327 (D) TOPOLOGY: LINEAR
328 (ii) MOLECULE TYPE: PEPTIDE
329 (ix) FEATURE:
330 (A) NAME/KEY: MOUSE iNOS (1002-1019)
331 (B) LOCATION:
332 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
333 (D) OTHER INFORMATION:
334 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
335
--> 336 ArgMetSerLeuValPheGlyCysArgHisProGluGlu
337 510
--> 338 AspHisLeuTyrGln
339 15
340
341

342 (2) INFORMATION FOR SEQ ID NO: 17:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:11

INPUT SET: S31225.raw

343 (i) SEQUENCE CHARACTERISTICS:
--> 344 (A) LENGTH: 16
345 (B) TYPE: AMINO ACID
346 (D) TOPOLOGY: LINEAR
347 (ii) MOLECULE TYPE: PEPTIDE
348 (ix) FEATURE:
349 (A) NAME/KEY: hnNOS [2-16, Cys17]
350 (B) LOCATION: HUMAN nNOS: AMINO TERMINAL
351 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
352 (D) OTHER INFORMATION:
353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
354
--> 355 GluAspHisMetPheGlyValGlnGlnIleGlnProAsn
356 510
--> 357 ValIleCys
358 15
359

360 (2) INFORMATION FOR SEQ ID NO: 18:
361 (i) SEQUENCE CHARACTERISTICS:
--> 362 (A) LENGTH: 24
363 (B) TYPE: AMINO ACID
364 (D) TOPOLOGY: LINEAR
365 (ii) MOLECULE TYPE: PEPTIDE
366 (ix) FEATURE:
367 (A) NAME/KEY: hnNOS [Cys1410-1411-1433]
368 (B) LOCATION: HUMAN nNOS: CARBOXYL TERMINAL
369 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
370 (D) OTHER INFORMATION:
371 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
372
--> 373 CysArgLeuArgSerGluSerIleAlaPheIleGluGlu
374 510
--> 375 SerLysLysAspThrAspGluValPheSerSer
376 1520
377
378

379 (2) INFORMATION FOR SEQ ID NO: 19:
380 (i) SEQUENCE CHARACTERISTICS:
--> 381 (A) LENGTH: 20
382 (B) TYPE: AMINO ACID
383 (D) TOPOLOGY: LINEAR
384 (ii) MOLECULE TYPE: PEPTIDE
385 (ix) FEATURE:
386 (A) NAME/KEY: hiNOS [2-21, Ser2]
387 (B) LOCATION: HUMAN iNOS: AMINO TERMINAL
388 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
389 (D) OTHER INFORMATION:
390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
391
--> 392 AlaSerProTrpLysPheLeuPheLysThrLysPheHis
393 510

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:11

INPUT SET: S31225.raw

--> 394 GlnTyrAlaMetAsnGlyGlu
395 1520
396
397

same

398 (2) INFORMATION FOR SEQ ID NO: 20:
399 (i) SEQUENCE CHARACTERISTICS:
--> 400 (A) LENGTH: 18
401 (B) TYPE: AMINO ACID
402 (D) TOPOLOGY: LINEAR
403 (ii) MOLECULE TYPE: PEPTIDE
404 (ix) FEATURE:
405 (A) NAME/KEY: hINOS [Cys1136-1137-1153]
406 (B) LOCATION: HUMAN iNOS: CARBOXYL TERMINAL
407 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
408 (D) OTHER INFORMATION:
409 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
410
411

--> 412 CysLysLysAspArgValAlaValGlnProSerSerLeu
413 510
--> 414 GluMetSerAlaLeu
415 15
416
417

418 (2) INFORMATION FOR SEQ ID NO: 21:
419 (i) SEQUENCE CHARACTERISTICS:
--> 420 (A) LENGTH: 12
421 (B) TYPE: AMINO ACID
422 (D) TOPOLOGY: LINEAR
423 (ii) MOLECULE TYPE: PEPTIDE
424 (ix) FEATURE:
425 (A) NAME/KEY: heNOS [Cap-2-12, Cys13]
426 (B) LOCATION: HUMAN eNOS: AMINO TERMINAL WITH CAPROIC ACID ATTACHED
427 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
428 (D) OTHER INFORMATION:
429 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
430
--> 431 GlyAsnLeuLysSerValAlaGlnGluProGlyCys
432 510
433
434

435 (2) INFORMATION FOR SEQ ID NO: 22:
436 (i) SEQUENCE CHARACTERISTICS:
--> 437 (A) LENGTH: 12
438 (B) TYPE: AMINO ACID
439 (D) TOPOLOGY: LINEAR
440 (ii) MOLECULE TYPE: PEPTIDE
441 (ix) FEATURE:
442 (A) NAME/KEY: heNOS [2-12, Cys13]
443 (B) LOCATION: HUMAN eNOS: AMINO TERMINAL WITHOUT CAPROIC ACID ATTACHED

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999

TIME: 08:48:12

INPUT SET: S31225.raw

444 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
445 (D) OTHER INFORMATION:
446 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
447
--> 448 GlyAsnLeuLysSerValAlaGlnGluProGlyCys
449 510
450
451

452 (2) INFORMATION FOR SEQ ID NO: 23:
453 (i) SEQUENCE CHARACTERISTICS:
--> 454 (A) LENGTH: 23
455 (B) TYPE: AMINO ACID
456 (D) TOPOLOGY: LINEAR
457 (ii) MOLECULE TYPE: PEPTIDE
458 (ix) FEATURE:
459 (A) NAME/KEY: heNOS [Cys1181-1182-1203]
460 (B) LOCATION: HUMAN eNOS: CARBOXYL TERMINAL
461 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
462 (D) OTHER INFORMATION:
463 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
464
--> 465 CysGluArgGlnLeuArgGluAlaValProTrpAlaPhe
466 510
--> 467 AspProProGlySerAspThrAsnSerPro
468 1520
469
470

471 (2) INFORMATION FOR SEQ ID NO: 24:
472 (i) SEQUENCE CHARACTERISTICS:
--> 473 (A) LENGTH: 18
474 (B) TYPE: AMINO ACID
475 (D) TOPOLOGY: LINEAR
476 (ii) MOLECULE TYPE: PEPTIDE
477 (ix) FEATURE:
478 (A) NAME/KEY: hiNOS [985-1002]
479 (B) LOCATION:
480 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
481 (D) OTHER INFORMATION:
482 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
483
--> 484 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
485 510
--> 486 HisAspSerGlnHis
487 15
488
489

490 (2) INFORMATION FOR SEQ ID NO: 25:
491 (i) SEQUENCE CHARACTERISTICS:
--> 492 (A) LENGTH: 18
493 (B) TYPE: AMINO ACID

same

✓

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:12

INPUT SET: S31225.raw

494 (D) TOPOLOGY: LINEAR
495 (ii) MOLECULE TYPE: PEPTIDE
496 (ix) FEATURE:
497 (A) NAME/KEY: hINOS [985-1002]
498 (B) LOCATION:
499 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
500 (D) OTHER INFORMATION:
501 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
502
--> 503 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
504 510
--> 505 His AspSerGlnHis
506 15
507
508

509 (2) INFORMATION FOR SEQ ID NO: 26:
510 (i) SEQUENCE CHARACTERISTICS:
--> 511 (A) LENGTH: 18
512 (B) TYPE: AMINO ACID
513 (D) TOPOLOGY: LINEAR
514 (ii) MOLECULE TYPE: PEPTIDE
515 (ix) FEATURE:
516 (A) NAME/KEY: hINOS [37-54]
517 (B) LOCATION:
518 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
519 (D) OTHER INFORMATION:
520 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
521
--> 522 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
523 510
--> 524 SerLysGlnGlnAsn
525 15
526
527

528 (2) INFORMATION FOR SEQ ID NO: 27:
529 (i) SEQUENCE CHARACTERISTICS:
--> 530 (A) LENGTH: 18
531 (B) TYPE: AMINO ACID
532 (D) TOPOLOGY: LINEAR
533 (ii) MOLECULE TYPE: PEPTIDE
534 (ix) FEATURE:
535 (A) NAME/KEY: hINOS [781-798]
536 (B) LOCATION:
537 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
538 (D) OTHER INFORMATION:
539 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
540
--> 541 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
542 510
543
--> 544 GlyProThrProHis

same

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RAW SEQUENCE LISTING
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INPUT SET: S31225.raw

545 15
546
547

548 (2) INFORMATION FOR SEQ ID NO: 28:
549 (i) SEQUENCE CHARACTERISTICS:
--> 550 (A) LENGTH: 18
551 (B) TYPE: AMINO ACID
552 (D) TOPOLOGY: LINEAR
553 (ii) MOLECULE TYPE: PEPTIDE
554 (ix) FEATURE:
555 (A) NAME/KEY: hiNOS [25-42]
556 (B) LOCATION:
557 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
558 (D) OTHER INFORMATION:
559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
560
--> 561 AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
562 510
--> 563 ProValThrGlnAsp
564 15
565
566

567 (2) INFORMATION FOR SEQ ID NO: 29:
568 (i) SEQUENCE CHARACTERISTICS:
--> 569 (A) LENGTH: 18
570 (B) TYPE: AMINO ACID
571 (D) TOPOLOGY: LINEAR
572 (ii) MOLECULE TYPE: PEPTIDE
573 (ix) FEATURE:
574 (A) NAME/KEY: hiNOS [37-54]
575 (B) LOCATION:
576 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
577 (D) OTHER INFORMATION:
578 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
579
--> 580 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
581 510
--> 582 SerLysGlnGlnAsn
583 15
584
585

586 (2) INFORMATION FOR SEQ ID NO: 30:
587 (i) SEQUENCE CHARACTERISTICS:
--> 588 (A) LENGTH: 18
589 (B) TYPE: AMINO ACID
590 (D) TOPOLOGY: LINEAR
591 (ii) MOLECULE TYPE: PEPTIDE
592 (ix) FEATURE:
593 (A) NAME/KEY: hiNOS [781-798]
594 (B) LOCATION:

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PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:13

INPUT SET: S31225.raw

595 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
596 (D) OTHER INFORMATION:
597 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
598

--> 599 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
600 510
--> 601 GlyProThrProHis
602 15
603
604

605 (2) INFORMATION FOR SEQ ID NO: 31:
606 (i) SEQUENCE CHARACTERISTICS:
--> 607 (A) LENGTH: 18
608 (B) TYPE: AMINO ACID
609 (D) TOPOLOGY: LINEAR
610 (ii) MOLECULE TYPE: PEPTIDE
611 (ix) FEATURE:
612 (A) NAME/KEY: hINOS [1009-1026]
613 (B) LOCATION:
614 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
615 (D) OTHER INFORMATION:
616 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
617
618

--> 619 ArgMetThrLeuValPheGlySerArgArgProAspGlu
620 510
--> 621 AspHisIleTyrGln
622 15
623
624

625 (2) INFORMATION FOR SEQ ID NO: 32:
626 (i) SEQUENCE CHARACTERISTICS:
--> 627 (A) LENGTH: 18
628 (B) TYPE: AMINO ACID
629 (D) TOPOLOGY: LINEAR
630 (ii) MOLECULE TYPE: PEPTIDE
631 (ix) FEATURE:
632 (A) NAME/KEY: (A3) LOCUS HUMAN iNOS (25-42)
633 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
634 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
635 (D) OTHER INFORMATION:
636 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
637

--> 638 AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
639 510
--> 640 ProValThrGlnAsp
641 15
642
643

644 (2) INFORMATION FOR SEQ ID NO: 33:

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PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:13

INPUT SET: S31225.raw

645 (i) SEQUENCE CHARACTERISTICS:
--> 646 (A) LENGTH: 18
647 (B) TYPE: AMINO ACID
648 (D) TOPOLOGY: LINEAR
649 (ii) MOLECULE TYPE: PEPTIDE
650 (ix) FEATURE:
651 (A) NAME/KEY: MOUSE iNOS (25-42)
652 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
653 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
654 (D) OTHER INFORMATION:
655 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
656
--> 657 AsnAsnAsnValLysLysThrProSerAlaValLeuSer
658 510
--> 659 ProThrIleGlnAsp
660 15
661
662

same

663 (2) INFORMATION FOR SEQ ID NO: 34:
--> 664 (i) SEQUENCE CHARACTERISTICS:
665 (A) LENGTH: 18
666 (B) TYPE: AMINO ACID
667 (D) TOPOLOGY: LINEAR
668 (ii) MOLECULE TYPE: PEPTIDE
669 (ix) FEATURE:
670 (A) NAME/KEY: RAT iNOS (25-42)
671 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
672 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
673 (D) OTHER INFORMATION:
674 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
675
--> 676 AsnAsnAsnValGluLysThrProGlyAlaIleProSer
677 510
--> 678 ProThrThrGlnAsp
679 15
680
681

682 (2) INFORMATION FOR SEQ ID NO: 35:
--> 683 (i) SEQUENCE CHARACTERISTICS:
684 (A) LENGTH: 15
685 (B) TYPE: AMINO ACID
686 (D) TOPOLOGY: LINEAR
687 (ii) MOLECULE TYPE: PEPTIDE
688 (ix) FEATURE:
689 (A) NAME/KEY: HUMAN iNOS (28-42)
690 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
691 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
692 (D) OTHER INFORMATION:
693 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
694
--> 695 ValGluLysAlaProSerAlaThrSerSerProValThr

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INPUT SET: S31225.raw

--> 696 510
697 GlnAsp
698 15
699
700

same

701 (2) INFORMATION FOR SEQ ID NO: 36:
702 (i) SEQUENCE CHARACTERISTICS:
--> 703 (A) LENGTH: 12
704 (B) TYPE: AMINO ACID
705 (D) TOPOLOGY: LINEAR
706 (ii) MOLECULE TYPE: PEPTIDE
707 (ix) FEATURE:
708 (A) NAME/KEY: HUMAN iNOS (31-42)
709 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
710 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
711 (D) OTHER INFORMATION:
712 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
713
--> 714 AlaProSerAlaThrSerSerProValThrGlnAsp
715 510
716
717

same

718 (2) INFORMATION FOR SEQ ID NO: 37:
719 (i) SEQUENCE CHARACTERISTICS:
--> 720 (A) LENGTH: 9
721 (B) TYPE: AMINO ACID
722 (D) TOPOLOGY: LINEAR
723 (ii) MOLECULE TYPE: PEPTIDE
724 (ix) FEATURE:
725 (A) NAME/KEY: HUMAN iNOS (34-42)
726 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
727 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
728 (D) OTHER INFORMATION:
729 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
730
--> 731 AlaThrSerSerProValThrGlnAsp
732 5
733
734

735 (2) INFORMATION FOR SEQ ID NO: 38:
736 (i) SEQUENCE CHARACTERISTICS:
--> 737 (A) LENGTH: 6
738 (B) TYPE: AMINO ACID
739 (D) TOPOLOGY: LINEAR
740 (ii) MOLECULE TYPE: PEPTIDE
741 (ix) FEATURE:
742 (A) NAME/KEY: HUMAN iNOS (37-42)
743 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
744 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
745 (D) OTHER INFORMATION:

same

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INPUT SET: S31225.raw

746 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
747
--> 748 SerProValThrGlnAsp
749 5
750
751

same

752 (2) INFORMATION FOR SEQ ID NO: 39:
753 (i) SEQUENCE CHARACTERISTICS:
--> 754 (A) LENGTH: 15
755 (B) TYPE: AMINO ACID
756 (D) TOPOLOGY: LINEAR
757 (ii) MOLECULE TYPE: PEPTIDE
758 (ix) FEATURE:
759 (A) NAME/KEY: HUMAN iNOS (25-39)
760 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
761 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
762 (D) OTHER INFORMATION:
763 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
764
--> 765 AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
766 510
--> 767 ProVal
768 15
769
770

771 (2) INFORMATION FOR SEQ ID NO: 40:
772 (i) SEQUENCE CHARACTERISTICS:
--> 773 (A) LENGTH: 12
774 (B) TYPE: AMINO ACID
775 (D) TOPOLOGY: LINEAR
776 (ii) MOLECULE TYPE: PEPTIDE
777 (ix) FEATURE:
778 (A) NAME/KEY: HUMAN iNOS (25-36)
779 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
780 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
781 (D) OTHER INFORMATION:
782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
783
--> 784 AsnAsnAsnValGluLysAlaProSerAlaThrSer
785 510
786
787

788 (2) INFORMATION FOR SEQ ID NO: 41:
789 (i) SEQUENCE CHARACTERISTICS:
--> 790 (A) LENGTH: 9
791 (B) TYPE: AMINO ACID
792 (D) TOPOLOGY: LINEAR
793 (ii) MOLECULE TYPE: PEPTIDE
794 (ix) FEATURE:
795 (A) NAME/KEY: HUMAN iNOS (25-33)

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796 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
797 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
798 (D) OTHER INFORMATION:
799 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
800
--> 801 AsnAsnAsnValGluLysAlaProSer
802 5
803
804

805 (2) INFORMATION FOR SEQ ID NO: 42:
806 (i) SEQUENCE CHARACTERISTICS:
--> 807 (A) LENGTH: 6
808 (B) TYPE: AMINO ACID
809 (D) TOPOLOGY: LINEAR
810 (ii) MOLECULE TYPE: PEPTIDE
811 (ix) FEATURE:
812 (A) NAME/KEY: HUMAN iNOS (25-30)
813 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
814 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
815 (D) OTHER INFORMATION:
816 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
817
--> 818 AsnAsnAsnValGluLys
819 5
820
821

822 (2) INFORMATION FOR SEQ ID NO: 43:
823 (i) SEQUENCE CHARACTERISTICS:
--> 824 (A) LENGTH: 18
825 (B) TYPE: AMINO ACID
826 (D) TOPOLOGY: LINEAR
827 (ii) MOLECULE TYPE: PEPTIDE
828 (ix) FEATURE:
829 (A) NAME/KEY: (A4) LOCUS HUMAN iNOS (37-54)
830 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
831 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
832 (D) OTHER INFORMATION:
833 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
834
--> 835 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
836 510
--> 837 SerLysGlnGlnAsn
838 15
839
840

841 (2) INFORMATION FOR SEQ ID NO: 44:
842 (i) SEQUENCE CHARACTERISTICS:
--> 843 (A) LENGTH: 15
844 (B) TYPE: AMINO ACID
845 (D) TOPOLOGY: LINEAR

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RAW SEQUENCE LISTING
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INPUT SET: S31225.raw

846 (ii) MOLECULE TYPE: PEPTIDE
847 (ix) FEATURE:
848 (A) NAME/KEY: HUMAN iNOS (40-54)
849 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
850 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
851 (D) OTHER INFORMATION:
852 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
853
--> 854 ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
855 510
--> 856 GlnAsn
857 15
858
859

860 (2) INFORMATION FOR SEQ ID NO: 45:
861 (i) SEQUENCE CHARACTERISTICS:
--> 862 (A) LENGTH: 12
863 (B) TYPE: AMINO ACID
864 (D) TOPOLOGY: LINEAR
865 (ii) MOLECULE TYPE: PEPTIDE
866 (ix) FEATURE:
867 (A) NAME/KEY: HUMAN iNOS (43-54)
868 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
869 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
870 (D) OTHER INFORMATION:
871 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
872
--> 873 AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
874 510
875
876
877
878

879 (2) INFORMATION FOR SEQ ID NO: 46:
880 (i) SEQUENCE CHARACTERISTICS:
--> 881 (A) LENGTH: 9
882 (B) TYPE: AMINO ACID
883 (D) TOPOLOGY: LINEAR
884 (ii) MOLECULE TYPE: PEPTIDE
885 (ix) FEATURE:
886 (A) NAME/KEY: HUMAN iNOS (46-54)
887 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
888 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
889 (D) OTHER INFORMATION:
890 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
891
--> 892 TyrHisAsnLeuSerLysGlnGlnAsn
893 5
894
895

896 (2) INFORMATION FOR SEQ ID NO: 47:

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PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
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INPUT SET: S31225.raw

897 (i) SEQUENCE CHARACTERISTICS:
--> 898 (A) LENGTH: 6
899 (B) TYPE: AMINO ACID
900 (D) TOPOLOGY: LINEAR
901 (ii) MOLECULE TYPE: PEPTIDE
902 (ix) FEATURE:
903 (A) NAME/KEY: HUMAN iNOS (49-54)
904 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
905 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
906 (D) OTHER INFORMATION:
907 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
908
--> 909 LeuSerLysGlnGlnAsn
910 5
911
912

913 (2) INFORMATION FOR SEQ ID NO: 48:
914 (i) SEQUENCE CHARACTERISTICS:
--> 915 (A) LENGTH: 15
916 (B) TYPE: AMINO ACID
917 (D) TOPOLOGY: LINEAR
918 (ii) MOLECULE TYPE: PEPTIDE
919 (ix) FEATURE:
920 (A) NAME/KEY: HUMAN iNOS (37-51)
921 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
922 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
923 (D) OTHER INFORMATION:
924 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
925
--> 926 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
927 510
--> 928 SerLys
929 15
930
931

932 (2) INFORMATION FOR SEQ ID NO: 49:
933 (i) SEQUENCE CHARACTERISTICS:
--> 934 (A) LENGTH: 12
935 (B) TYPE: AMINO ACID
936 (D) TOPOLOGY: LINEAR
937 (ii) MOLECULE TYPE: PEPTIDE
938 (ix) FEATURE:
939 (A) NAME/KEY: HUMAN iNOS (37-48)
940 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
941 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
942 (D) OTHER INFORMATION:
943 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
944
--> 945 SerProValThrGlnAspAspLeuGlnTyrHisAsn
946 510
947

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PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
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INPUT SET: S31225.raw

948

949 (2) INFORMATION FOR SEQ ID NO: 50:
950 (i) SEQUENCE CHARACTERISTICS:
--> 951 (A) LENGTH: 9
952 (B) TYPE: AMINO ACID
953 (D) TOPOLOGY: LINEAR
954 (ii) MOLECULE TYPE: PEPTIDE
955 (ix) FEATURE:
956 (A) NAME/KEY: HUMAN iNOS (37-45)
957 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
958 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
959 (D) OTHER INFORMATION:
960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
961
--> 962 SerProValThrGlnAspAspLeuGln
963 5
964
965

966 (2) INFORMATION FOR SEQ ID NO: 51:
967 (i) SEQUENCE CHARACTERISTICS:
--> 968 (A) LENGTH: 6
969 (B) TYPE: AMINO ACID
970 (D) TOPOLOGY: LINEAR
971 (ii) MOLECULE TYPE: PEPTIDE
972 (ix) FEATURE:
973 (A) NAME/KEY: HUMAN iNOS (37-42)
974 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
975 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
976 (D) OTHER INFORMATION:
977 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:
978
--> 979 SerProValThrGlnAsp
980 5
981
982
983

984 (2) INFORMATION FOR SEQ ID NO: 52:
985 (i) SEQUENCE CHARACTERISTICS:
--> 986 (A) LENGTH: 18
987 (B) TYPE: AMINO ACID
988 (D) TOPOLOGY: LINEAR
989 (ii) MOLECULE TYPE: PEPTIDE
990 (ix) FEATURE:
991 (A) NAME/KEY: (F6) LOCUS HUMAN iNOS (781-798)
992 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
993 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
994 (D) OTHER INFORMATION:
995 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:
996
--> 997 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp

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INPUT SET: S31225.raw

998 510
--> 999 GlyProThrProHis
1000 15
1001
1002

1003 (2) INFORMATION FOR SEQ ID NO: 53:
1004 (i) SEQUENCE CHARACTERISTICS:
--> 1005 (A) LENGTH: 19
1006 (B) TYPE: AMINO ACID
1007 (D) TOPOLOGY: LINEAR
1008 (ii) MOLECULE TYPE: PEPTIDE
1009 (ix) FEATURE:
1010 (A) NAME/KEY: HUMAN eNOS (806-824)
1011 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1012 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1013 (D) OTHER INFORMATION:
1014 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:
1015
--> 1016 ProGlyLeuValGluAlaLeuLeuSerArgValGluAsp
1017 510
--> 1018 ProProAlaProThrGlu
1019 15
1020
1021

1022 (2) INFORMATION FOR SEQ ID NO: 54:
1023 (i) SEQUENCE CHARACTERISTICS:
--> 1024 (A) LENGTH: 15
1025 (B) TYPE: AMINO ACID
1026 (D) TOPOLOGY: LINEAR
1027 (ii) MOLECULE TYPE: PEPTIDE
1028 (ix) FEATURE:
1029 (A) NAME/KEY: HUMAN iNOS (784-798)
1030 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1031 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1032 (D) OTHER INFORMATION:
1033 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:
1034
1035
--> 1036 ValGlnGlyIleLeuGluArgValValAspGlyProThr
1037 510
--> 1038 ProHis
1039 15
1040
1041

1042 (2) INFORMATION FOR SEQ ID NO: 55:
1043 (i) SEQUENCE CHARACTERISTICS:
--> 1044 (A) LENGTH: 12
1045 (B) TYPE: AMINO ACID
1046 (D) TOPOLOGY: LINEAR
1047 (ii) MOLECULE TYPE: PEPTIDE

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PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:16

INPUT SET: S31225.raw

1048 (ix) FEATURE:
1049 (A) NAME/KEY: HUMAN iNOS (787-798)
1050 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1051 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1052 (D) OTHER INFORMATION:
1053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
1054
--> 1055 IleLeuGluArgValValAspGlyProThrProHis
1056 510
1057
1058

1059 (2) INFORMATION FOR SEQ ID NO: 56:
1060 (i) SEQUENCE CHARACTERISTICS:
--> 1061 (A) LENGTH: 9
1062 (B) TYPE: AMINO ACID
1063 (D) TOPOLOGY: LINEAR
1064 (ii) MOLECULE TYPE: PEPTIDE
1065 (ix) FEATURE:
1066 (A) NAME/KEY: HUMAN iNOS (790-798)
1067 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1068 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1069 (D) OTHER INFORMATION:
1070 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
1071
--> 1072 ArgValValAspGlyProThrProHis
1073 5
1074
1075

1076 (2) INFORMATION FOR SEQ ID NO: 57:
1077 (i) SEQUENCE CHARACTERISTICS:
--> 1078 (A) LENGTH: 6
1079 (B) TYPE: AMINO ACID
1080 (D) TOPOLOGY: LINEAR
1081 (ii) MOLECULE TYPE: PEPTIDE
1082 (ix) FEATURE:
1083 (A) NAME/KEY: HUMAN iNOS (793-798)
1084 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1085 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1086 (D) OTHER INFORMATION:
1087 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
1088
--> 1089 AspGlyProThrProHis
1090 5
1091
1092

1093 (2) INFORMATION FOR SEQ ID NO: 58:
1094 (i) SEQUENCE CHARACTERISTICS:
--> 1095 (A) LENGTH: 14
1096 (B) TYPE: AMINO ACID
1097 (D) TOPOLOGY: LINEAR

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INPUT SET: S31225.raw

1098 (ii) MOLECULE TYPE: PEPTIDE
1099 (ix) FEATURE:
1100 (A) NAME/KEY: HUMAN iNOS (781-794)
1101 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1102 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1103 (D) OTHER INFORMATION:
1104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
1105
--> 1106 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
1107 510
1108 Gly
1109
1110

1111 (2) INFORMATION FOR SEQ ID NO: 59:
1112 (i) SEQUENCE CHARACTERISTICS:
--> 1113 (A) LENGTH: 12
1114 (B) TYPE: AMINO ACID
1115 (D) TOPOLOGY: LINEAR
1116 (ii) MOLECULE TYPE: PEPTIDE
1117 (ix) FEATURE:
1118 (A) NAME/KEY: HUMAN iNOS (781-792)
1119 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1120 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1121 (D) OTHER INFORMATION:
1122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
1123
--> 1124 ProAlaLeuValGlnGlyIleLeuGluArgValVal
1125 510
1126
1127

1128 (2) INFORMATION FOR SEQ ID NO: 60:
1129 (i) SEQUENCE CHARACTERISTICS:
--> 1130 (A) LENGTH: 9
1131 (B) TYPE: AMINO ACID
1132 (D) TOPOLOGY: LINEAR
1133 (ii) MOLECULE TYPE: PEPTIDE
1134 (ix) FEATURE:
1135 (A) NAME/KEY: HUMAN iNOS (781-789)
1136 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1137 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1138 (D) OTHER INFORMATION:
1139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:
1140
--> 1141 ProAlaLeuValGlnGlyIleLeuGlu
1142 5
1143
1144

1145 (2) INFORMATION FOR SEQ ID NO: 61:
1146 (i) SEQUENCE CHARACTERISTICS:
--> 1147 (A) LENGTH: 6

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1148 (B) TYPE: AMINO ACID
1149 (D) TOPOLOGY: LINEAR
1150 (ii) MOLECULE TYPE: PEPTIDE
1151 (ix) FEATURE:
1152 (A) NAME/KEY: HUMAN iNOS (781-786)
1153 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1154 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1155 (D) OTHER INFORMATION:
1156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:
1157
--> 1158 ProAlaLeuValGlnGly
1159 5
1160
1161

1162 (2) INFORMATION FOR SEQ ID NO: 62:
1163 (i) SEQUENCE CHARACTERISTICS:
--> 1164 (A) LENGTH: 18
1165 (B) TYPE: AMINO ACID
1166 (D) TOPOLOGY: LINEAR
1167 (ii) MOLECULE TYPE: PEPTIDE
1168 (ix) FEATURE:
1169 (A) NAME/KEY: (G11) LOCUS HUMAN iNOS (985-1002)
1170 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1171 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1172 (D) OTHER INFORMATION:
1173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:
1174
--> 1175 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1176 510
--> 1177 HisAspSerGlnHis
1178 15
1179
1180

1181 (2) INFORMATION FOR SEQ ID NO: 63:
1182 (i) SEQUENCE CHARACTERISTICS:
--> 1183 (A) LENGTH: 18
1184 (B) TYPE: AMINO ACID
1185 (D) TOPOLOGY: LINEAR
1186 (ii) MOLECULE TYPE: PEPTIDE
1187 (ix) FEATURE:
1188 (A) NAME/KEY: HUMAN nNOS (1256-1273)
1189 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1190 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1191 (D) OTHER INFORMATION:
1192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:
1193
--> 1194 GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
1195 510
--> 1196 PheAspIleGlnHis
1197 15
1198

same

↓

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1199

1200 (2) INFORMATION FOR SEQ ID NO: 64:
1201 (i) SEQUENCE CHARACTERISTICS:
--> 1202 (A) LENGTH: 15
1203 (B) TYPE: AMINO ACID
1204 (D) TOPOLOGY: LINEAR
1205 (ii) MOLECULE TYPE: PEPTIDE
1206 (ix) FEATURE:
1207 (A) NAME/KEY: HUMAN eNOS (1017-1031)
1208 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1209 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1210 (D) OTHER INFORMATION:
1211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
1212
--> 1213 GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
1214 510
--> 1215 HisAsp
1216 15
1217
1218

1219 (2) INFORMATION FOR SEQ ID NO: 65:
1220 (i) SEQUENCE CHARACTERISTICS:
--> 1221 (A) LENGTH: 15
1222 (B) TYPE: AMINO ACID
1223 (D) TOPOLOGY: LINEAR
1224 (ii) MOLECULE TYPE: PEPTIDE
1225 (ix) FEATURE:
1226 (A) NAME/KEY: HUMAN iNOS (988-1002)
1227 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1228 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1229 (D) OTHER INFORMATION:
1230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:
1231
--> 1232 ProPheArgSerPheTrpGlnGlnArgLeuHisAspSer
1233 510
--> 1234 GlnHis
1235 15
1236
1237

1238 (2) INFORMATION FOR SEQ ID NO: 66:
1239 (i) SEQUENCE CHARACTERISTICS:
--> 1240 (A) LENGTH: 12
1241 (B) TYPE: AMINO ACID
1242 (D) TOPOLOGY: LINEAR
1243 (ii) MOLECULE TYPE: PEPTIDE
1244 (ix) FEATURE:
1245 (A) NAME/KEY: HUMAN iNOS (991-1002)
1246 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1247 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1248 (D) OTHER INFORMATION:

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1249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:
1250
--> 1251 SerPheTrpGlnGlnArgLeuHisAspSerGlnHis
1252 510
1253
1254

1255 (2) INFORMATION FOR SEQ ID NO: 67:
1256 (i) SEQUENCE CHARACTERISTICS:
--> 1257 (A) LENGTH: 9
1258 (B) TYPE: AMINO ACID
1259 (D) TOPOLOGY: LINEAR
1260 (ii) MOLECULE TYPE: PEPTIDE
1261 (ix) FEATURE:
1262 (A) NAME/KEY: HUMAN iNOS (994-1002)
1263 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1264 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1265 (D) OTHER INFORMATION:
1266 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:
1267
--> 1268 GlnGlnArgLeuHisAspSerGlnHis
1269 5
1270
1271

1272 (2) INFORMATION FOR SEQ ID NO: 68:
1273 (i) SEQUENCE CHARACTERISTICS:
--> 1274 (A) LENGTH: 5
1275 (B) TYPE: AMINO ACID
1276 (D) TOPOLOGY: LINEAR
1277 (ii) MOLECULE TYPE: PEPTIDE
1278 (ix) FEATURE:
1279 (A) NAME/KEY: HUMAN iNOS (997-1002)
1280 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1281 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1282 (D) OTHER INFORMATION:
1283 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:
1284
--> 1285 HisAspSerGlnHis
1286 5
1287
1288

1289 (2) INFORMATION FOR SEQ ID NO: 69:
1290 (i) SEQUENCE CHARACTERISTICS:
--> 1291 (A) LENGTH: 15
1292 (B) TYPE: AMINO ACID
1293 (D) TOPOLOGY: LINEAR
1294 (ii) MOLECULE TYPE: PEPTIDE
1295 (ix) FEATURE:
1296 (A) NAME/KEY: HUMAN iNOS (985-998)
1297 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1298 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS

same

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1299 (D) OTHER INFORMATION:
1300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:
1301
--> 1302 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1303 510
--> 1304 HisAsp
1305 15
1306
1307

1308 (2) INFORMATION FOR SEQ ID NO: 70:
1309 (i) SEQUENCE CHARACTERISTICS:
--> 1310 (A) LENGTH: 12
1311 (B) TYPE: AMINO ACID
1312 (D) TOPOLOGY: LINEAR
1313 (ii) MOLECULE TYPE: PEPTIDE
1314 (ix) FEATURE:
1315 (A) NAME/KEY: HUMAN iNOS (985-996)
1316 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1317 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1318 (D) OTHER INFORMATION:
1319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:
1320
--> 1321 GlyIleValProPheArgSerPheTrpGlnGlnArg
1322 510
1323
1324

1325 (2) INFORMATION FOR SEQ ID NO: 71:
1326 (i) SEQUENCE CHARACTERISTICS:
--> 1327 (A) LENGTH: 9
1328 (B) TYPE: AMINO ACID
1329 (D) TOPOLOGY: LINEAR
1330 (ii) MOLECULE TYPE: PEPTIDE
1331 (ix) FEATURE:
1332 (A) NAME/KEY: HUMAN iNOS (985-993)
1333 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1334 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1335 (D) OTHER INFORMATION:
1336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:
1337
--> 1338 GlyIleValProPheArgSerPheTrp
1339 5
1340
1341

1342 (2) INFORMATION FOR SEQ ID NO: 72:
1343 (i) SEQUENCE CHARACTERISTICS:
--> 1344 (A) LENGTH: 6
1345 (B) TYPE: AMINO ACID
1346 (D) TOPOLOGY: LINEAR
1347 (ii) MOLECULE TYPE: PEPTIDE
1348 (ix) FEATURE:

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1349 (A) NAME/KEY: HUMAN iNOS (985-990)
1350 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1351 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1352 (D) OTHER INFORMATION:
1353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:
1354
--> 1355 GlyIleValProPheArg
1356 5
1357
1358

1359 (2) INFORMATION FOR SEQ ID NO: 73:
1360 (i) SEQUENCE CHARACTERISTICS:
--> 1361 (A) LENGTH: 18
1362 (B) TYPE: AMINO ACID
1363 (D) TOPOLOGY: LINEAR
1364 (ii) MOLECULE TYPE: PEPTIDE
1365 (ix) FEATURE:
1366 (A) NAME/KEY: (H1) LOCUS HUMAN iNOS (1009-1026)
1367 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1368 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1369 (D) OTHER INFORMATION:
1370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:
1371
--> 1372 ArgMetThrLeuValPheGlySerArgArgProAspGlu
1373 510
--> 1374 AspHisIleTyrGln
1375 15
1376
1377

1378 (2) INFORMATION FOR SEQ ID NO: 74:
1379 (i) SEQUENCE CHARACTERISTICS:
--> 1380 (A) LENGTH: 17
1381 (B) TYPE: AMINO ACID
1382 (D) TOPOLOGY: LINEAR
1383 (ii) MOLECULE TYPE: PEPTIDE
1384 (ix) FEATURE:
1385 (A) NAME/KEY: HUMAN eNOS (1041-1057)
1386 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1387 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1388 (D) OTHER INFORMATION:
1389 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:
1390
--> 1391 MetThrLeuValPheGlySerArgSerSerGlnLeuAsp
1392 510
--> 1393 HisLeuTyrArg
1394 15
1395
1396

1397 (2) INFORMATION FOR SEQ ID NO: 75:
1398 (i) SEQUENCE CHARACTERISTICS:

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--> 1399 (A) LENGTH: 17
1400 (B) TYPE: AMINO ACID
1401 (D) TOPOLOGY: LINEAR
1402 (ii) MOLECULE TYPE: PEPTIDE
1403 (ix) FEATURE:
1404 (A) NAME/KEY: HUMAN nNOS (1281-1297)
1405 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1406 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1407 (D) OTHER INFORMATION:
1408 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:
1409

--> 1410 MetValLeuValPheGlySerArgGlnSerLysIleAsp
1411 510
--> 1412 HisIleTyrArg
1413 15
1414
1415

1416 (2) INFORMATION FOR SEQ ID NO: 76:
1417 (i) SEQUENCE CHARACTERISTICS:
--> 1418 (A) LENGTH: 15
1419 (B) TYPE: AMINO ACID
1420 (D) TOPOLOGY: LINEAR
1421 (ii) MOLECULE TYPE: PEPTIDE
1422 (ix) FEATURE:
1423 (A) NAME/KEY: HUMAN iNOS (1012-1026)
1424 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1425 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1426 (D) OTHER INFORMATION:
1427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:
1428
--> 1429 LeuValPheGlySerArgArgProAspGluAspHisIle
1430 510
--> 1431 TyrGln
1432 15
1433
1434

1435 (2) INFORMATION FOR SEQ ID NO: 77:
1436 (i) SEQUENCE CHARACTERISTICS:
--> 1437 (A) LENGTH: 12
1438 (B) TYPE: AMINO ACID
1439 (D) TOPOLOGY: LINEAR
1440 (ii) MOLECULE TYPE: PEPTIDE
1441 (ix) FEATURE:
1442 (A) NAME/KEY: HUMAN iNOS (1015-1026)
1443 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1444 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1445 (D) OTHER INFORMATION:
1446 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:
1447
--> 1448 GlySerArgArgProAspGluAspHisIleTyrGln
1449 510

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1450
1451
1452
1453

1454 (2) INFORMATION FOR SEQ ID NO: 78:
1455 (i) SEQUENCE CHARACTERISTICS:
--> 1456 (A) LENGTH: 9
1457 (B) TYPE: AMINO ACID
1458 (D) TOPOLOGY: LINEAR
1459 (ii) MOLECULE TYPE: PEPTIDE
1460 (ix) FEATURE:
1461 (A) NAME/KEY: HUMAN iNOS (1018-1026)
1462 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1463 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1464 (D) OTHER INFORMATION:
1465 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:
1466
--> 1467 ArgProAspGluAspHisIleTyrGln
1468 5
1469
1470

1471 (2) INFORMATION FOR SEQ ID NO: 79:
1472 (i) SEQUENCE CHARACTERISTICS:
--> 1473 (A) LENGTH: 6
1474 (B) TYPE: AMINO ACID
1475 (D) TOPOLOGY: LINEAR
1476 (ii) MOLECULE TYPE: PEPTIDE
1477 (ix) FEATURE:
1478 (A) NAME/KEY: HUMAN iNOS (1021-1026)
1479 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1480 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1481 (D) OTHER INFORMATION:
1482 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:
1483
--> 1484 GluAspHisIleTyrGln
1485 5
1486
1487

1488 (2) INFORMATION FOR SEQ ID NO: 80:
1489 (i) SEQUENCE CHARACTERISTICS:
--> 1490 (A) LENGTH: 15
1491 (B) TYPE: AMINO ACID
1492 (D) TOPOLOGY: LINEAR
1493 (ii) MOLECULE TYPE: PEPTIDE
1494 (ix) FEATURE:
1495 (A) NAME/KEY: HUMAN iNOS (1009-1023)
1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1497 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1498 (D) OTHER INFORMATION:
1499 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

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1500
--> 1501 ArgMetThrLeuValPheGlySerArgArgProAspGlu
1502 510
--> 1503 AspHis
1504 15
1505
1506

1507 (2) INFORMATION FOR SEQ ID NO: 81:
1508 (i) SEQUENCE CHARACTERISTICS:
--> 1509 (A) LENGTH: 11
1510 (B) TYPE: AMINO ACID
1511 (D) TOPOLOGY: LINEAR
1512 (ii) MOLECULE TYPE: PEPTIDE
1513 (ix) FEATURE:
1514 (A) NAME/KEY: HUMAN iNOS (1009-1020)
1515 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1516 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1517 (D) OTHER INFORMATION:
1518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:
1519
--> 1520 ArgMetThrLeuValPheGlySerArgArgPro
1521 510
1522
1523

1524 (2) INFORMATION FOR SEQ ID NO: 82:
1525 (i) SEQUENCE CHARACTERISTICS:
--> 1526 (A) LENGTH: 9
1527 (B) TYPE: AMINO ACID
1528 (D) TOPOLOGY: LINEAR
1529 (ii) MOLECULE TYPE: PEPTIDE
1530 (ix) FEATURE:
1531 (A) NAME/KEY: HUMAN iNOS (1009-1017)
1532 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1533 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1534 (D) OTHER INFORMATION:
1535 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
1536
--> 1537 ArgMetThrLeuValPheGlySerArg-amide
1538 5
1539
1540

1541 (2) INFORMATION FOR SEQ ID NO: 83:
1542 (i) SEQUENCE CHARACTERISTICS:
--> 1543 (A) LENGTH: 6
1544 (B) TYPE: AMINO ACID
1545 (D) TOPOLOGY: LINEAR
1546 (ii) MOLECULE TYPE: PEPTIDE
1547 (ix) FEATURE:
1548 (A) NAME/KEY: HUMAN iNOS (1009-1014)
1549 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE

*only amino acids
are shown
in the
sequence itself*

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1550 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1551 (D) OTHER INFORMATION:
1552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:
1553
--> 1554 ArgMetThrLeuValPhe-amide
1555 5
1556
1557
1558

1559 (2) INFORMATION FOR SEQ ID NO: 84:
1560 (i) SEQUENCE CHARACTERISTICS:
--> 1561 (A) LENGTH: 12
1562 (B) TYPE: AMINO ACID
1563 (D) TOPOLOGY: LINEAR
1564 (ii) MOLECULE TYPE: PEPTIDE
1565 (ix) FEATURE:
1566 (A) NAME/KEY: TRUNCATED HUMAN INOS (40-54)
1567 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1568 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1569 (D) OTHER INFORMATION:
1570 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:
1571
--> 1572 ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLys
1573 510
1574
1575

1576 (2) INFORMATION FOR SEQ ID NO: 85:
1577 (i) SEQUENCE CHARACTERISTICS:
--> 1578 (A) LENGTH: 9
1579 (B) TYPE: AMINO ACID
1580 (D) TOPOLOGY: LINEAR
1581 (ii) MOLECULE TYPE: PEPTIDE
1582 (ix) FEATURE:
1583 (A) NAME/KEY: TRUNCATED HUMAN INOS (784-798)
1584 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1585 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1586 (D) OTHER INFORMATION:
1587 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:
1588
--> 1589 ValGlnGlyIleLeuGluArgValVal
1590 5
1591
1592

1593 (2) INFORMATION FOR SEQ ID NO: 86:
1594 (i) SEQUENCE CHARACTERISTICS:
--> 1595 (A) LENGTH: 18
1596 (B) TYPE: AMINO ACID
1597 (D) TOPOLOGY: LINEAR
1598 (ii) MOLECULE TYPE: PEPTIDE
1599 (ix) FEATURE:

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1600 (A) NAME/KEY: HUMAN iNOS (37-54)
1601 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1602 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1603 (D) OTHER INFORMATION:
1604 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:
1605
--> 1606 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1607 510
--> 1608 SerLysGlnGlnAsn
1609 15
1610
1611

1612 (2) INFORMATION FOR SEQ ID NO: 87:
1613 (i) SEQUENCE CHARACTERISTICS:
--> 1614 (A) LENGTH: 5
1615 (B) TYPE: AMINO ACID
1616 (D) TOPOLOGY: LINEAR
1617 (ii) MOLECULE TYPE: PEPTIDE
1618 (ix) FEATURE:
1619 (A) NAME/KEY: HUMAN iNOS (41-45)
1620 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1621 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1622 (D) OTHER INFORMATION:
1623 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:
1624
--> 1625 GlnAspAspLeuGln
1626 5
1627
1628

1629 (2) INFORMATION FOR SEQ ID NO: 88:
1630 (i) SEQUENCE CHARACTERISTICS:
--> 1631 (A) LENGTH: 6
1632 (B) TYPE: AMINO ACID
1633 (D) TOPOLOGY: LINEAR
1634 (ii) MOLECULE TYPE: PEPTIDE
1635 (ix) FEATURE:
1636 (A) NAME/KEY: HUMAN iNOS (40-45)
1637 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1638 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1639 (D) OTHER INFORMATION:
1640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:
1641
--> 1642 ThrGlnAspAspLeuGln
1643 5
1644
1645

1646 (2) INFORMATION FOR SEQ ID NO: 89:
1647 (i) SEQUENCE CHARACTERISTICS:
--> 1648 (A) LENGTH: 7
1649 (B) TYPE: AMINO ACID

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1650 (D) TOPOLOGY: LINEAR
1651 (ii) MOLECULE TYPE: PEPTIDE
1652 (ix) FEATURE:
1653 (A) NAME/KEY: HUMAN iNOS (39-45)
1654 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1655 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1656 (D) OTHER INFORMATION:
1657 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:
1658
--> 1659 ValThrGlnAspAspLeuGln
1660 5
1661
1662
1663
1664

1665 (2) INFORMATION FOR SEQ ID NO: 90:
1666 (i) SEQUENCE CHARACTERISTICS:
--> 1667 (A) LENGTH: 8
1668 (B) TYPE: AMINO ACID
1669 (D) TOPOLOGY: LINEAR
1670 (ii) MOLECULE TYPE: PEPTIDE
1671 (ix) FEATURE:
1672 (A) NAME/KEY: HUMAN iNOS (38-45)
1673 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1674 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1675 (D) OTHER INFORMATION:
1676 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:
1677
--> 1678 ProValThrGlnAspAspLeuGln
1679 5
1680
1681

1682 (2) INFORMATION FOR SEQ ID NO: 91:
1683 (i) SEQUENCE CHARACTERISTICS:
--> 1684 (A) LENGTH: 9
1685 (B) TYPE: AMINO ACID
1686 (D) TOPOLOGY: LINEAR
1687 (ii) MOLECULE TYPE: PEPTIDE
1688 (ix) FEATURE:
1689 (A) NAME/KEY: HUMAN iNOS (37-45)
1690 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1691 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1692 (D) OTHER INFORMATION:
1693 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:
1694
--> 1695 SerProValThrGlnAspAspLeuGln
1696 5
1697
1698

1699 (2) INFORMATION FOR SEQ ID NO: 92:

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INPUT SET: S31225.raw

1700 (i) SEQUENCE CHARACTERISTICS:
--> 1701 (A) LENGTH: 5
1702 (B) TYPE: AMINO ACID
1703 (D) TOPOLOGY: LINEAR
1704 (ii) MOLECULE TYPE: PEPTIDE
1705 (ix) FEATURE:
1706 (A) NAME/KEY: HUMAN iNOS (40-44)
1707 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1708 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1709 (D) OTHER INFORMATION:
1710 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
1711
--> 1712 ThrGlnAspAspLeu
1713 5
1714
1715
1716

1717 (2) INFORMATION FOR SEQ ID NO: 93:
1718 (i) SEQUENCE CHARACTERISTICS:
--> 1719 (A) LENGTH: 6
1720 (B) TYPE: AMINO ACID
1721 (D) TOPOLOGY: LINEAR
1722 (ii) MOLECULE TYPE: PEPTIDE
1723 (ix) FEATURE:
1724 (A) NAME/KEY: HUMAN iNOS (39-44)
1725 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1726 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1727 (D) OTHER INFORMATION:
1728 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:
1729
--> 1730 ValThrGlnAspAspLeu
1731 5
1732
1733

1734 (2) INFORMATION FOR SEQ ID NO: 94:
1735 (i) SEQUENCE CHARACTERISTICS:
--> 1736 (A) LENGTH: 7
1737 (B) TYPE: AMINO ACID
1738 (D) TOPOLOGY: LINEAR
1739 (ii) MOLECULE TYPE: PEPTIDE
1740 (ix) FEATURE:
1741 (A) NAME/KEY: HUMAN iNOS (38-44)
1742 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1743 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1744 (D) OTHER INFORMATION:
1745 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:
1746
--> 1747 ProValThrGlnAspAspLeu
1748 5
1749
1750

RAW SEQUENCE LISTING
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1751 (2) INFORMATION FOR SEQ ID NO: 95:
1752 (i) SEQUENCE CHARACTERISTICS:
--> 1753 (A) LENGTH: 8
1754 (B) TYPE: AMINO ACID
1755 (D) TOPOLOGY: LINEAR
1756 (ii) MOLECULE TYPE: PEPTIDE
1757 (ix) FEATURE:
1758 (A) NAME/KEY: HUMAN iNOS (37-44)
1759 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1760 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1761 (D) OTHER INFORMATION:
1762 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
1763
--> 1764 SerProValThrGlnAspAspLeu
1765 5
1766
1767
1768

1769 (2) INFORMATION FOR SEQ ID NO: 96:
1770 (i) SEQUENCE CHARACTERISTICS:
--> 1771 (A) LENGTH: 9
1772 (B) TYPE: AMINO ACID
1773 (D) TOPOLOGY: LINEAR
1774 (ii) MOLECULE TYPE: PEPTIDE
1775 (ix) FEATURE:
1776 (A) NAME/KEY: HUMAN iNOS (36-44)
1777 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1778 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1779 (D) OTHER INFORMATION:
1780 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:
1781
--> 1782 SerSerProValThrGlnAspAspLeu
1783 5
1784
1785

1786 (2) INFORMATION FOR SEQ ID NO: 97:
1787 (i) SEQUENCE CHARACTERISTICS:
--> 1788 (A) LENGTH: 5
1789 (B) TYPE: AMINO ACID
1790 (D) TOPOLOGY: LINEAR
1791 (ii) MOLECULE TYPE: PEPTIDE
1792 (ix) FEATURE:
1793 (A) NAME/KEY: HUMAN iNOS (39-43)
1794 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1795 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1796 (D) OTHER INFORMATION:
1797 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:
1798
--> 1799 ValThrGlnAspAsp
1800 5

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1801
1802

1803 (2) INFORMATION FOR SEQ ID NO: 98:
1804 (i) SEQUENCE CHARACTERISTICS:
--> 1805 (A) LENGTH: 6
1806 (B) TYPE: AMINO ACID
1807 (D) TOPOLOGY: LINEAR
1808 (ii) MOLECULE TYPE: PEPTIDE
1809 (ix) FEATURE:
1810 (A) NAME/KEY: HUMAN iNOS (38-43)
1811 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1812 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1813 (D) OTHER INFORMATION:
1814 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:
1815
--> 1816 ProValThrGlnAspAsp
1817 5
1818
1819
1820

1821 (2) INFORMATION FOR SEQ ID NO: 99:
1822 (i) SEQUENCE CHARACTERISTICS:
--> 1823 (A) LENGTH: 7
1824 (B) TYPE: AMINO ACID
1825 (D) TOPOLOGY: LINEAR
1826 (ii) MOLECULE TYPE: PEPTIDE
1827 (ix) FEATURE:
1828 (A) NAME/KEY: HUMAN iNOS (37-43)
1829 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1830 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1831 (D) OTHER INFORMATION:
1832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:
1833
--> 1834 SerProValThrGlnAspAsp
1835 5
1836
1837

1838 (2) INFORMATION FOR SEQ ID NO: 100:
1839 (i) SEQUENCE CHARACTERISTICS:
--> 1840 (A) LENGTH: 8
1841 (B) TYPE: AMINO ACID
1842 (D) TOPOLOGY: LINEAR
1843 (ii) MOLECULE TYPE: PEPTIDE
1844 (ix) FEATURE:
1845 (A) NAME/KEY: HUMAN iNOS (36-43)
1846 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1847 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1848 (D) OTHER INFORMATION:
1849 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:
1850

same



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--> 1851 SerSerProValThrGlnAspAsp
1852 5
1853
1854

1855 (2) INFORMATION FOR SEQ ID NO: 101:
1856 (i) SEQUENCE CHARACTERISTICS:
--> 1857 (A) LENGTH: 9
1858 (B) TYPE: AMINO ACID
1859 (D) TOPOLOGY: LINEAR
1860 (ii) MOLECULE TYPE: PEPTIDE
1861 (ix) FEATURE:
1862 (A) NAME/KEY: HUMAN iNOS (35-43)
1863 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1864 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1865 (D) OTHER INFORMATION:
1866 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:
1867
--> 1868 ThrSerSerProValThrGlnAspAsp
1869 5
1870
1871
1872

1873 (2) INFORMATION FOR SEQ ID NO: 102:
1874 (i) SEQUENCE CHARACTERISTICS:
--> 1875 (A) LENGTH: 18
1876 (B) TYPE: AMINO ACID
1877 (D) TOPOLOGY: LINEAR
1878 (ii) MOLECULE TYPE: PEPTIDE
1879 (ix) FEATURE:
1880 (A) NAME/KEY: HUMAN iNOS (37-54)
1881 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1882 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1883 (D) OTHER INFORMATION:
1884 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:
1885
--> 1886 SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1887 510
--> 1888 SerLysGlnGlnAsn
1889 15
1890
1891

1892 (2) INFORMATION FOR SEQ ID NO: 103:
1893 (i) SEQUENCE CHARACTERISTICS:
--> 1894 (A) LENGTH: 15
1895 (B) TYPE: AMINO ACID
1896 (D) TOPOLOGY: LINEAR
1897 (ii) MOLECULE TYPE: PEPTIDE
1898 (ix) FEATURE:
1899 (A) NAME/KEY: HUMAN iNOS (40-54)
1900 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE

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1901 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1902 (D) OTHER INFORMATION:
1903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:
1904
--> 1905 ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
1906 510
--> 1907 GlnAsn
1908 15
1909
1910

1911 (2) INFORMATION FOR SEQ ID NO: 104:
1912 (i) SEQUENCE CHARACTERISTICS:
--> 1913 (A) LENGTH: 12
1914 (B) TYPE: AMINO ACID
1915 (D) TOPOLOGY: LINEAR
1916 (ii) MOLECULE TYPE: PEPTIDE
1917 (ix) FEATURE:
1918 (A) NAME/KEY: HUMAN iNOS (43-54)
1919 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1920 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1921 (D) OTHER INFORMATION:
1922 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:
1923
1924
--> 1925 AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
1926 510
1927
1928

1929 (2) INFORMATION FOR SEQ ID NO: 105:
1930 (i) SEQUENCE CHARACTERISTICS:
--> 1931 (A) LENGTH: 9
1932 (B) TYPE: AMINO ACID
1933 (D) TOPOLOGY: LINEAR
1934 (ii) MOLECULE TYPE: PEPTIDE
1935 (ix) FEATURE:
1936 (A) NAME/KEY: HUMAN iNOS (46-54)
1937 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1938 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1939 (D) OTHER INFORMATION:
1940 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:
1941
--> 1942 TyrHisAsnLeuSerLysGlnGlnAsn
1943 5
1944
1945

1946 (2) INFORMATION FOR SEQ ID NO: 106:
1947 (i) SEQUENCE CHARACTERISTICS:
--> 1948 (A) LENGTH: 6
1949 (B) TYPE: AMINO ACID
1950 (D) TOPOLOGY: LINEAR

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1951 (ii) MOLECULE TYPE: PEPTIDE
1952 (ix) FEATURE:
1953 (A) NAME/KEY: HUMAN iNOS (49-54)
1954 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1955 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1956 (D) OTHER INFORMATION:
1957 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
1958
--> 1959 **LeuSerLysGlnGlnAsn**
1960 5
1961
1962

1963 (2) INFORMATION FOR SEQ ID NO: 107:
1964 (i) SEQUENCE CHARACTERISTICS:
--> 1965 (A) **LENGTH: 15**
1966 (B) TYPE: AMINO ACID
1967 (D) TOPOLOGY: LINEAR
1968 (ii) MOLECULE TYPE: PEPTIDE
1969 (ix) FEATURE:
1970 (A) NAME/KEY: HUMAN iNOS (37-51)
1971 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1972 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1973 (D) OTHER INFORMATION:
1974 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
1975
--> 1976 **SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu**
1977 510
--> 1978 **SerLys**
1979 15
1980
1981

1982 (2) INFORMATION FOR SEQ ID NO: 108:
1983 (i) SEQUENCE CHARACTERISTICS:
--> 1984 (A) **LENGTH: 12**
1985 (B) TYPE: AMINO ACID
1986 (D) TOPOLOGY: LINEAR
1987 (ii) MOLECULE TYPE: PEPTIDE
1988 (ix) FEATURE:
1989 (A) NAME/KEY: HUMAN iNOS (37-48)
1990 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1991 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1992 (D) OTHER INFORMATION:
1993 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
1994
--> 1995 **SerProValThrGlnAspAspLeuGlnTyrHisAsn**
1996 510
1997
1998

1999 (2) INFORMATION FOR SEQ ID NO: 109:
2000 (i) SEQUENCE CHARACTERISTICS:

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--> 2001 (A) LENGTH: 9
2002 (B) TYPE: AMINO ACID
2003 (D) TOPOLOGY: LINEAR
2004 (ii) MOLECULE TYPE: PEPTIDE
2005 (ix) FEATURE:
2006 (A) NAME/KEY: HUMAN iNOS (37-45)
2007 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2008 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2009 (D) OTHER INFORMATION:
2010 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:
2011

--> 2012 SerProValThrGlnAspAspLeuGln
2013 5
2014
2015

2016 (2) INFORMATION FOR SEQ ID NO: 110:
2017 (i) SEQUENCE CHARACTERISTICS:
--> 2018 (A) LENGTH: 6
2019 (B) TYPE: AMINO ACID
2020 (D) TOPOLOGY: LINEAR
2021 (ii) MOLECULE TYPE: PEPTIDE
2022 (ix) FEATURE:
2023 (A) NAME/KEY: HUMAN iNOS (37-42)
2024 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2025 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2026 (D) OTHER INFORMATION:
2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:
2028
2029

--> 2030 SerProValThrGlnAsp
2031 5
2032
2033

2034 (2) INFORMATION FOR SEQ ID NO: 111:
2035 (i) SEQUENCE CHARACTERISTICS:
--> 2036 (A) LENGTH: 10
2037 (B) TYPE: AMINO ACID
2038 (D) TOPOLOGY: LINEAR
2039 (ii) MOLECULE TYPE: PEPTIDE
2040 (ix) FEATURE:
2041 (A) NAME/KEY: HUMAN iNOS (35-44)
2042 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2043 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2044 (D) OTHER INFORMATION:
2045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:
2046

--> 2047 ThrSerSerProValThrGlnAspAspLeu
2048 510
2049
2050

2051 (2) INFORMATION FOR SEQ ID NO: 112:

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2103
2104

2105 (2) INFORMATION FOR SEQ ID NO: 115:
2106 (i) SEQUENCE CHARACTERISTICS:
--> 2107 (A) LENGTH: 7
2108 (B) TYPE: AMINO ACID
2109 (D) TOPOLOGY: LINEAR
2110 (ii) MOLECULE TYPE: PEPTIDE
2111 (ix) FEATURE:
2112 (A) NAME/KEY: HUMAN INOS (786-792)
2113 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2114 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2115 (D) OTHER INFORMATION:
2116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:
2117
--> 2118 GlyIleLeuGluArgValVal
2119 5
2120
2121

2122 (2) INFORMATION FOR SEQ ID NO: 116:
2123 (i) SEQUENCE CHARACTERISTICS:
--> 2124 (A) LENGTH: 8
2125 (B) TYPE: AMINO ACID
2126 (D) TOPOLOGY: LINEAR
2127 (ii) MOLECULE TYPE: PEPTIDE
2128 (ix) FEATURE:
2129 (A) NAME/KEY: HUMAN INOS (785-792)
2130 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2131 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2132 (D) OTHER INFORMATION:
2133
2134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:
2135
--> 2136 GlnGlyIleLeuGluArgValVal
2137 5
2138
2139

2140 (2) INFORMATION FOR SEQ ID NO: 117:
2141 (i) SEQUENCE CHARACTERISTICS:
--> 2142 (A) LENGTH: 9
2143 (B) TYPE: AMINO ACID
2144 (D) TOPOLOGY: LINEAR
2145 (ii) MOLECULE TYPE: PEPTIDE
2146 (ix) FEATURE:
2147 (A) NAME/KEY: HUMAN INOS (784-792)
2148 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2149 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2150 (D) OTHER INFORMATION:
2151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
2152

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2052 (i) SEQUENCE CHARACTERISTICS:
--> 2053 (A) LENGTH: 18
2054 (B) TYPE: AMINO ACID
2055 (D) TOPOLOGY: LINEAR
2056 (ii) MOLECULE TYPE: PEPTIDE
2057 (ix) FEATURE:
2058 (A) NAME/KEY: HUMAN iNOS (781-798)
2059 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2060 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2061 (D) OTHER INFORMATION:
2062 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
2063
--> 2064 ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
2065 510
--> 2066 GlyProThrProHis
2067 15
2068
2069

2070 (2) INFORMATION FOR SEQ ID NO: 113:
2071 (i) SEQUENCE CHARACTERISTICS:
--> 2072 (A) LENGTH: 5
2073 (B) TYPE: AMINO ACID
2074 (D) TOPOLOGY: LINEAR
2075 (ii) MOLECULE TYPE: PEPTIDE
2076 (ix) FEATURE:
2077 (A) NAME/KEY: HUMAN iNOS (788-792)
2078 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2079 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2080 (D) OTHER INFORMATION:
2081
2082 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
2083
--> 2084 LeuGluArgValVal
2085 5
2086
2087

2088 (2) INFORMATION FOR SEQ ID NO: 114:
2089 (i) SEQUENCE CHARACTERISTICS:
--> 2090 (A) LENGTH: 6
2091 (B) TYPE: AMINO ACID
2092 (D) TOPOLOGY: LINEAR
2093 (ii) MOLECULE TYPE: PEPTIDE
2094 (ix) FEATURE:
2095 (A) NAME/KEY: HUMAN iNOS (787-792)
2096 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2097 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2098 (D) OTHER INFORMATION:
2099 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:
2100
--> 2101 IleLeuGluArgValVal
2102 5

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--> 2153 ValGlnGlyIleLeuGluArgValVal
2154 5
2155
2156

same

2157 (2) INFORMATION FOR SEQ ID NO: 118:
2158 (i) SEQUENCE CHARACTERISTICS:
--> 2159 (A) LENGTH: 5
2160 (B) TYPE: AMINO ACID
2161 (D) TOPOLOGY: LINEAR
2162 (ii) MOLECULE TYPE: PEPTIDE
2163 (ix) FEATURE:
2164 (A) NAME/KEY: HUMAN iNOS (787-791)
2165 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2166 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2167 (D) OTHER INFORMATION:
2168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:
2169
--> 2170 IleLeuGluArgVal
2171 5
2172
2173

2174 (2) INFORMATION FOR SEQ ID NO: 119:
2175 (i) SEQUENCE CHARACTERISTICS:
--> 2176 (A) LENGTH: 6
2177 (B) TYPE: AMINO ACID
2178 (D) TOPOLOGY: LINEAR
2179 (ii) MOLECULE TYPE: PEPTIDE
2180 (ix) FEATURE:
2181 (A) NAME/KEY: HUMAN iNOS (786-791)
2182 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2183 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2184 (D) OTHER INFORMATION:
2185
2186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:
2187
--> 2188 GlyIleLeuGluArgVal
2189 5
2190
2191

2192 (2) INFORMATION FOR SEQ ID NO: 120:
2193 (i) SEQUENCE CHARACTERISTICS:
--> 2194 (A) LENGTH: 7
2195 (B) TYPE: AMINO ACID
2196 (D) TOPOLOGY: LINEAR
2197 (ii) MOLECULE TYPE: PEPTIDE
2198 (ix) FEATURE:
2199 (A) NAME/KEY: HUMAN iNOS (785-791)
2200 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2201 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2202 (D) OTHER INFORMATION:

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2203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:
2204
--> 2205 GlnGlyIleLeuGluArgVal
2206 5
2207
2208

2209 (2) INFORMATION FOR SEQ ID NO: 121:
2210 (i) SEQUENCE CHARACTERISTICS:
--> 2211 (A) LENGTH: 8
2212 (B) TYPE: AMINO ACID
2213 (D) TOPOLOGY: LINEAR
2214 (ii) MOLECULE TYPE: PEPTIDE
2215 (ix) FEATURE:
2216 (A) NAME/KEY: HUMAN iNOS (784-791)
2217 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2218 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2219 (D) OTHER INFORMATION:
2220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:
2221
--> 2222 ValGlnGlyIleLeuGluArgVal
2223 5
2224
2225

2226 (2) INFORMATION FOR SEQ ID NO: 122:
2227 (i) SEQUENCE CHARACTERISTICS:
--> 2228 (A) LENGTH: 9
2229 (B) TYPE: AMINO ACID
2230 (D) TOPOLOGY: LINEAR
2231 (ii) MOLECULE TYPE: PEPTIDE
2232 (ix) FEATURE:
2233 (A) NAME/KEY: HUMAN iNOS (783-791)
2234 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2235 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2236 (D) OTHER INFORMATION:
2237
2238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:
2239
--> 2240 LeuValGlnGlyIleLeuGluArgVal
2241 5
2242
2243

2244 (2) INFORMATION FOR SEQ ID NO: 123:
2245 (i) SEQUENCE CHARACTERISTICS:
--> 2246 (A) LENGTH: 5
2247 (B) TYPE: AMINO ACID
2248 (D) TOPOLOGY: LINEAR
2249 (ii) MOLECULE TYPE: PEPTIDE
2250 (ix) FEATURE:
2251 (A) NAME/KEY: HUMAN iNOS (786-790)
2252 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE

*same**✓*

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2253 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2254 (D) OTHER INFORMATION:
2255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:
2256
--> 2257 GlyIleLeuGluArg
2258 5
2259
2260

2261 (2) INFORMATION FOR SEQ ID NO: 124:
2262 (i) SEQUENCE CHARACTERISTICS:
--> 2263 (A) LENGTH: 6
2264 (B) TYPE: AMINO ACID
2265 (D) TOPOLOGY: LINEAR
2266 (ii) MOLECULE TYPE: PEPTIDE
2267 (ix) FEATURE:
2268 (A) NAME/KEY: HUMAN iNOS (785-790)
2269 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2270 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2271 (D) OTHER INFORMATION:
2272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:
2273
--> 2274 GlnGlyIleLeuGluArg
2275 5
2276
2277

2278 (2) INFORMATION FOR SEQ ID NO: 125:
2279 (i) SEQUENCE CHARACTERISTICS:
--> 2280 (A) LENGTH: 7
2281 (B) TYPE: AMINO ACID
2282 (D) TOPOLOGY: LINEAR
2283 (ii) MOLECULE TYPE: PEPTIDE
2284 (ix) FEATURE:
2285 (A) NAME/KEY: HUMAN iNOS (784-790)
2286 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2287 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2288 (D) OTHER INFORMATION:
2289
2290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:
2291
--> 2292 ValGlnGlyIleLeuGluArg
2293 5
2294
2295

2296 (2) INFORMATION FOR SEQ ID NO: 126:
2297 (i) SEQUENCE CHARACTERISTICS:
--> 2298 (A) LENGTH: 8
2299 (B) TYPE: AMINO ACID
2300 (D) TOPOLOGY: LINEAR
2301 (ii) MOLECULE TYPE: PEPTIDE
2302 (ix) FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:25

INPUT SET: S31225.raw

2303 (A) NAME/KEY: HUMAN iNOS (783-790)
2304 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2305 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2306 (D) OTHER INFORMATION:
2307
2308 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
2309
--> 2310 LeuValGlnGlyIleLeuGluArg
2311 5
2312
--> 2313 ?? Delete at end of file
2314
2315
2316
2317
2318
2319
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2321
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2325
2326

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999
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INPUT SET: S31225.raw

Line	Error	Original Text
20	Wrong application Serial Number	(A) APPLICATION NUMBER: NONE
37	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
50	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProCysAlaThrSerSer
52	Wrong Amino Acid Designator	ProValThrGlnAsp
58	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
69	Wrong Amino Acid Designator	AsnAsnAsnValLysLysThrProCysAlaValLeuSer
71	Wrong Amino Acid Designator	ProThrIleGlnAsp
77	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
88	Wrong Amino Acid Designator	AsnAsnAsnValGluLysThrProGlyAlalleProSer
90	Wrong Amino Acid Designator	ProThrThrGlnAsp
96	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
107	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
109	Wrong Amino Acid Designator	SerLysGlnGlnAsn
115	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
126	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
128	Wrong Amino Acid Designator	GlyProThrProHis
134	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17
145	Wrong Amino Acid Designator	XaaAlaLeuValGlnGlyIleLeuGluArgValValAsp
147	Wrong Amino Acid Designator	CysProThrProHis
154	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
165	Wrong Amino Acid Designator	XaaXaaLeuValGlnGlyIleLeuGluArgValValAsp
167	Wrong Amino Acid Designator	CysSerSerProXaa
173	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
184	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
186	Wrong Amino Acid Designator	HisAspSerGlnHis
192	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
204	Wrong Amino Acid Designator	GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu
206	Wrong Amino Acid Designator	HisAspSerGlnHis
212	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
223	Wrong Amino Acid Designator	GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu510
224	Wrong Amino Acid Designator	HisAspSerGlnHis
230	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
241	Wrong Amino Acid Designator	GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
243	Wrong Amino Acid Designator	PheAspIleGlnHis
249	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
260	Wrong Amino Acid Designator	GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
262	Wrong Amino Acid Designator	HisAspXaaXaaXaa
268	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
279	Wrong Amino Acid Designator	GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
281	Wrong Amino Acid Designator	HisAspXaaXaaXaa
287	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
298	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlyCysArgArgProAspGlu
300	Wrong Amino Acid Designator	AspHisIleTyrGln
306	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
317	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlyCysArgHisProGluGlu
319	Wrong Amino Acid Designator	AspHisLeuTyrGln
325	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
336	Wrong Amino Acid Designator	ArgMetSerLeuValPheGlyCysArgHisProGluGlu

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PATENT APPLICATION US/08/833,506A

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Line	Error	Original Text
338	Wrong Amino Acid Designator	AspHisLeuTyrGln
344	Entered (16) and Calc. Seq. Length (0) differ	(A) LENGTH: 16
355	Wrong Amino Acid Designator	GluAspHisMetPheGlyValGlnGlnIleGlnProAsn
357	Wrong Amino Acid Designator	VallIleCys
362	Entered (24) and Calc. Seq. Length (0) differ	(A) LENGTH: 24
373	Wrong Amino Acid Designator	CysArgLeuArgSerGluSerIleAlaPhelleGluGlu
375	Wrong Amino Acid Designator	SerLysLysAspThrAspGluValPheSerSer
381	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20
392	Wrong Amino Acid Designator	AlaSerProTrpLysPheLeuPheLysThrLysPheHis
394	Wrong Amino Acid Designator	GlnTyrAlaMetAsnGlyGlu
400	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
412	Wrong Amino Acid Designator	CysLysLysAspArgValAlaValGlnProSerSerLeu
414	Wrong Amino Acid Designator	GluMetSerAlaLeu
420	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
431	Wrong Amino Acid Designator	GlyAsnLeuLysSerValAlaGlnGluProGlyCys
437	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
448	Wrong Amino Acid Designator	GlyAsnLeuLysSerValAlaGlnGluProGlyCys
454	Entered (23) and Calc. Seq. Length (0) differ	(A) LENGTH: 23
465	Wrong Amino Acid Designator	CysGluArgGlnLeuArgGluAlaValProTrpAlaPhe
467	Wrong Amino Acid Designator	AspProProGlySerAspThrAsnSerPro
473	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
484	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
486	Wrong Amino Acid Designator	HisAspSerGlnHis
492	Entered (18) and Calc. Seq. Length (1) differ	(A) LENGTH: 18
503	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
505	Wrong Amino Acid Designator	His AspSerGlnHis
511	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
522	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
524	Wrong Amino Acid Designator	SerLysGlnGlnAsn
530	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
541	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
544	Wrong Amino Acid Designator	GlyProThrProHis
550	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
561	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
563	Wrong Amino Acid Designator	ProValThrGlnAsp
569	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
580	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
582	Wrong Amino Acid Designator	SerLysGlnGlnAsn
588	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
599	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
601	Wrong Amino Acid Designator	GlyProThrProHis
607	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
619	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgProAspGlu
621	Wrong Amino Acid Designator	AspHisIleTyrGln
627	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
638	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
640	Wrong Amino Acid Designator	ProValThrGlnAsp
646	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18

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Line	Error	Original Text
657	Wrong Amino Acid Designator	AsnAsnAsnValLysLysThrProSerAlaValLeuSer
659	Wrong Amino Acid Designator	ProThrIleGlnAsp
665	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
676	Wrong Amino Acid Designator	AsnAsnAsnValGluLysThrProGlyAlaIleProSer
678	Wrong Amino Acid Designator	ProThrThrGlnAsp
684	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
695	Wrong Amino Acid Designator	ValGluLysAlaProSerAlaThrSerSerProValThr
697	Wrong Amino Acid Designator	GlnAsp
703	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
714	Wrong Amino Acid Designator	AlaProSerAlaThrSerSerProValThrGlnAsp
720	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
731	Wrong Amino Acid Designator	AlaThrSerSerProValThrGlnAsp
737	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
748	Wrong Amino Acid Designator	SerProValThrGlnAsp
754	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
765	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
767	Wrong Amino Acid Designator	ProVal
773	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
784	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSer
790	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
801	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSer
807	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
818	Wrong Amino Acid Designator	AsnAsnAsnValGluLys
824	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
835	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
837	Wrong Amino Acid Designator	SerLysGlnGlnAsn
843	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
854	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
856	Wrong Amino Acid Designator	GlnAsn
862	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
873	Wrong Amino Acid Designator	AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
881	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
892	Wrong Amino Acid Designator	TyrHisAsnLeuSerLysGlnGlnAsn
898	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
909	Wrong Amino Acid Designator	LeuSerLysGlnGlnAsn
915	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
926	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
928	Wrong Amino Acid Designator	SerLys
934	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
945	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsn
951	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
962	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGln
968	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
979	Wrong Amino Acid Designator	SerProValThrGlnAsp
986	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
997	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
999	Wrong Amino Acid Designator	GlyProThrProHis
1005	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19

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INPUT SET: S31225.raw

Line	Error	Original Text
1016	Wrong Amino Acid Designator	ProGlyLeuValGluAlaLeuLeuSerArgValGluAsp
1018	Wrong Amino Acid Designator	ProProAlaProThrGlu
1024	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1036	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgValValAspGlyProThr
1038	Wrong Amino Acid Designator	ProHis
1044	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1055	Wrong Amino Acid Designator	IleLeuGluArgValValAspGlyProThrProHis
1061	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1072	Wrong Amino Acid Designator	ArgValValAspGlyProThrProHis
1078	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1089	Wrong Amino Acid Designator	AspGlyProThrProHis
1095	Entered (14) and Calc. Seq. Length (1) differ	(A) LENGTH: 14
1106	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
1113	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1124	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValVal
1130	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1141	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGlu
1147	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1158	Wrong Amino Acid Designator	ProAlaLeuValGlnGly
1164	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1175	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1177	Wrong Amino Acid Designator	HisAspSerGlnHis
1183	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1194	Wrong Amino Acid Designator	GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
1196	Wrong Amino Acid Designator	PheAspIleGlnHis
1202	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1213	Wrong Amino Acid Designator	GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
1215	Wrong Amino Acid Designator	HisAsp
1221	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1232	Wrong Amino Acid Designator	ProPheArgSerPheTrpGlnGlnArgLeuHisAspSer
1234	Wrong Amino Acid Designator	GlnHis
1240	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1251	Wrong Amino Acid Designator	SerPheTrpGlnGlnArgLeuHisAspSerGlnHis
1257	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1268	Wrong Amino Acid Designator	GlnGlnArgLeuHisAspSerGlnHis
1274	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1285	Wrong Amino Acid Designator	HisAspSerGlnHis
1291	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1302	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1304	Wrong Amino Acid Designator	HisAsp
1310	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1321	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArg
1327	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1338	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrp
1344	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1355	Wrong Amino Acid Designator	GlyIleValProPheArg
1361	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1372	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgProAspGlu

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INPUT SET: S31225.raw

Line	Error	Original Text
1374	Wrong Amino Acid Designator	AspHisIleTyrGln
1380	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17
1391	Wrong Amino Acid Designator	MetThrLeuValPheGlySerArgSerSerGlnLeuAsp
1393	Wrong Amino Acid Designator	HisLeuTyrArg
1399	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17
1410	Wrong Amino Acid Designator	MetValLeuValPheGlySerArgGlnSerLysIleAsp
1412	Wrong Amino Acid Designator	HisIleTyrArg
1418	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1429	Wrong Amino Acid Designator	LeuValPheGlySerArgArgProAspGluAspHisIle
1431	Wrong Amino Acid Designator	TyrGln
1437	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1448	Wrong Amino Acid Designator	GlySerArgArgProAspGluAspHisIleTyrGln
1456	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1467	Wrong Amino Acid Designator	ArgProAspGluAspHisIleTyrGln
1473	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1484	Wrong Amino Acid Designator	GluAspHisIleTyrGln
1490	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1501	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgProAspGlu
1503	Wrong Amino Acid Designator	AspHis
1509	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH: 11
1520	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgPro
1526	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1537	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArg-amide
1543	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1554	Wrong Amino Acid Designator	ArgMetThrLeuValPhe-amide
1561	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1572	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLys
1578	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1589	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgValVal
1595	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1606	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1608	Wrong Amino Acid Designator	SerLysGlnGlnAsn
1614	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1625	Wrong Amino Acid Designator	GlnAspAspLeuGln
1631	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1642	Wrong Amino Acid Designator	ThrGlnAspAspLeuGln
1648	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1659	Wrong Amino Acid Designator	ValThrGlnAspAspLeuGln
1667	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1678	Wrong Amino Acid Designator	ProValThrGlnAspAspLeuGln
1684	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1695	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGln
1701	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1712	Wrong Amino Acid Designator	ThrGlnAspAspLeu
1719	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1730	Wrong Amino Acid Designator	ValThrGlnAspAspLeu
1736	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1747	Wrong Amino Acid Designator	ProValThrGlnAspAspLeu

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Line	Error	Original Text
1753	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1764	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeu
1771	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1782	Wrong Amino Acid Designator	SerSerProValThrGlnAspAspLeu
1788	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1799	Wrong Amino Acid Designator	ValThrGlnAspAsp
1805	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1816	Wrong Amino Acid Designator	ProValThrGlnAspAsp
1823	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1834	Wrong Amino Acid Designator	SerProValThrGlnAspAsp
1840	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1851	Wrong Amino Acid Designator	SerSerProValThrGlnAspAsp
1857	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1868	Wrong Amino Acid Designator	ThrSerSerProValThrGlnAspAsp
1875	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1886	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1888	Wrong Amino Acid Designator	SerLysGlnGlnAsn
1894	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1905	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
1907	Wrong Amino Acid Designator	GlnAsn
1913	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1925	Wrong Amino Acid Designator	AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
1931	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1942	Wrong Amino Acid Designator	TyrHisAsnLeuSerLysGlnGlnAsn
1948	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1959	Wrong Amino Acid Designator	LeuSerLysGlnGlnAsn
1965	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1976	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1978	Wrong Amino Acid Designator	SerLys
1984	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1995	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsn
2001	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
2012	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGln
2018	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2030	Wrong Amino Acid Designator	SerProValThrGlnAsp
2036	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10
2047	Wrong Amino Acid Designator	ThrSerSerProValThrGlnAspAspLeu
2053	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
2064	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
2066	Wrong Amino Acid Designator	GlyProThrProHis
2072	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
2084	Wrong Amino Acid Designator	LeuGluArgValVal
2090	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2101	Wrong Amino Acid Designator	IleLeuGluArgValVal
2107	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
2118	Wrong Amino Acid Designator	GlyIleLeuGluArgValVal
2124	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
2136	Wrong Amino Acid Designator	GlnGlyIleLeuGluArgValVal

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/833,506ADATE: 03/29/1999
TIME: 08:48:27

INPUT SET: S31225.raw

Line	Error	Original Text
2142	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
2153	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgValVal
2159	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
2170	Wrong Amino Acid Designator	IleLeuGluArgVal
2176	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2188	Wrong Amino Acid Designator	GlyIleLeuGluArgVal
2194	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
2205	Wrong Amino Acid Designator	GlnGlyIleLeuGluArgVal
2211	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
2222	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgVal
2228	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
2240	Wrong Amino Acid Designator	LeuValGlnGlyIleLeuGluArgVal
2246	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
2257	Wrong Amino Acid Designator	GlyIleLeuGluArg
2263	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2274	Wrong Amino Acid Designator	GlnGlyIleLeuGluArg
2280	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
2292	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArg
2298	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
2310	Wrong Amino Acid Designator	LeuValGlnGlyIleLeuGluArg
2313	Wrong Amino Acid Designator	??